BLAST search against



Identify gene family

ClustalW comparison with SwissProt top hit



Demonstrates global

BLAST against nonredundant GPCR db



Demonstrates GPCR sub-

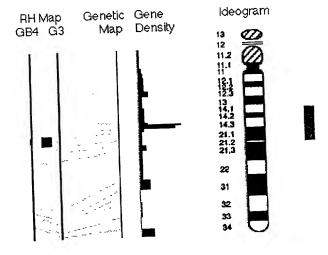
Figure 2

ClustalW Alignment of PFI-017 with Cysteinyl Leukotriene Receptor

		1							70
PFI-017	(1)								NVFMLNLAISDL
CysLT1	(1)	MDETGNLT	VSSATCI	IDTIDDFRNÇ	VYSTLYS	MISVVGF	FGNGFVLYVI	IKTYHKKSAF	QVYMINLAVADL
Consensus	(1)	MD G S	S	TID FK	F LY	II G	GNG IYV	I Y K SA	NVFMINLAIADL
		71							140
PFI-017	(70)	6.88	PM T0000	2000 - VIII.	7 3800 800.7		4 ₁₀₀ 000000 ₄ 5,7000 7 20000 1	2000 2000-	FRLLHVTSIRSA
CysLT1	(71)	LCVCTLPL	RVVYYVI	KGIWLFGDE	LCRLST	ALYVNLY	CSIFFMTAMS	FFRCIAIVF	VQNINLVTQKKA
Consensus	(71)	L I TLP	R YYL	WIFGD	CRI SY	YALYVNLY	SIFFLT LS	R IAIV F	ILSKA
		141							210
PFI-017	(140)	WILCGIIW	ILIMASS	IMLLDSGSE	QN-GSV	SCLELNL	YKIAK L QI	MNYTALVVGC	LLPFFTLSICYL
CysLT1	(141)	RFVCVGIW	IF VI LTS	SPFLMAKPO	KDEKNN	KČFEPPQ:	DNQTKNHVLV	LHY VS LFVGF	IIPFVIIIVCYT
Consensus	(141)	LC IW	I II S	LA	7	CE	K L	L YIAL VG	IIPF I ICY
		211							280
PFI-017	(207)								KDRLHKALV
CysLT1	(211)	MIILTLLK	KSMKKN-	-LSSHKKA]	GMIMVV	AAFLVSF	M PYHIQRTIH	LHFLHNETKE	CDSVLRMQKSVV
Consensus	(211)	TII TTK	M	SHKKAI	III	F L F	LPYH RTIH	L	C RL KALV
		281						_	40
PFI-017	(273)	ITLALAAA	NAČFNĚI	JYYFAGENE	KDRLKSA	LRKGHPQ:	KAKTKCVFPV	SVWLRKETRV	<i>7</i>
CysLT1	(279)	ITLELAAS	NCCEDPI	LYFFSGGNE	RKRLS-1	FRKHSLS	SVTYVPRKKA	SLPEKGEEIC	KV
Consensus	(281)	ITLALAAA	V CF PI	LYFFAG NF	K RL	RK		SL K E	

Figure 3

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Figure 4

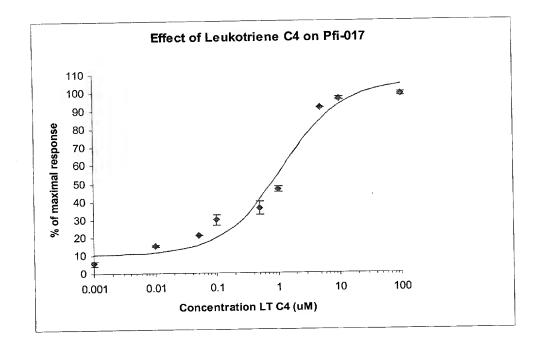
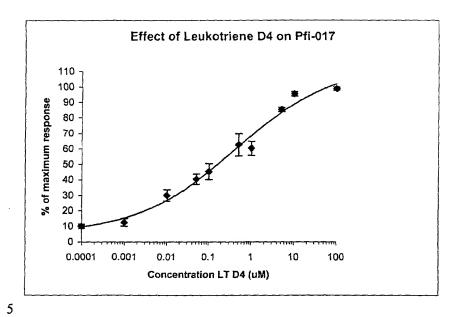


Figure 5



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Figure 6A

(SEQ ID NO: 1)

Figure 6B

(SEQ ID NO: 2)

Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr lle Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val Ser Val Trp Leu Arg Lys Glu Thr Arg Val

Figure 7A

(SEQ ID NO: 5)

Figure 7B

(SEQ ID NO: 6)

Met Glu Arg Lys Phe Met Ser Leu Gln Pro Ser Ile Ser Val Ser Glu Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu Tvr Tvr Phe Ala Glv Glu Asn Phe Lvs Asp Arg Leu Lvs Ser Ala Leu Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val Ser Val Trp Leu Arg Lys Glu Thr Arg Val